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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 17:00:49 ; Search time 194.042 Seconds
(without alignments)
10829.323 Million cell updates/sec

Title: US-09-497-967-102

Perfect score: 1410

Sequence: 1 atgaagaacaacatcctggt.....cttactacctgtgtaataa 1410

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2773584 seqs, 745158349 residues

Total number of hits satisfying chosen parameters: 5547168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	35.8	2.5	2017	6	US-10-293-865-17
C 2	35.4	2.5	4863	1	PCT-1102-00904-30
C 3	34.4	2.4	584	5	US-09-531-113-11107
C 4	34.4	2.4	2110	6	US-10-225-567A-505
C 5	34.4	2.4	37716	1	PCT-US02-32727-48
C 6	34.4	2.4	37716	6	US-10-057-498-48
C 7	34.4	2.4	555	6	US-10-144-771-26535
C 8	34.4	2.4	1215	1	PCT-US02-40225-2140
C 9	34.4	2.4	1215	6	US-10-320-797-2140
C 10	33.8	2.4	6692	6	US-10-144-771-38397
C 11	33.6	2.4	849	5	US-09-724-676-19769
C 12	33.6	2.4	849	5	US-09-724-676-19769
C 13	33.6	2.4	2161	5	US-09-620-312D-1053
C 14	33.6	2.4	2194	1	PCT-US02-40718-11
C 15	33.6	2.4	2230	5	US-09-620-312D-1052
C 16	33.2	2.4	1009	6	US-10-144-779-651
C 17	33.2	2.4	1077	6	US-10-144-771-43535
C 18	33.2	2.4	1234	6	US-10-144-771-1344
C 19	33.2	2.4	3008	6	US-10-144-779-75
C 20	32.8	2.3	256	5	US-09-531-113-26707
C 21	32.8	2.3	495	5	US-09-531-113-3673
C 22	32.8	2.3	500	5	US-09-531-113-5605
C 23	32.8	2.3	1082	6	US-10-144-771-14722
C 24	32.8	2.3	3912	6	US-10-144-771-4901
C 25	32.6	2.3	537	7	US-60-436-643-2181
C 26	32.6	2.3	3606	6	US-10-144-771-41270

C 27	32.4	2.3	17014	6	US-10-144-771-30161
C 28	32.2	2.3	251	5	US-09-531-113-28384
C 29	32.2	2.3	5271	5	US-09-949-004-511
C 30	32.2	2.3	6315	5	US-09-949-004-615
C 31	32.2	2.3	6358	5	US-09-949-004-616
C 32	32.2	2.3	21003	6	US-10-017-161-1039
C 33	32	2.3	279	1	PCT-US02-40891-1483
C 34	32	2.3	432	5	US-09-513-999C-1867
C 35	32	2.3	1070	6	US-10-342-887-1352
C 36	32	2.3	1109	5	US-09-620-312D-775
C 37	32	2.3	21719	1	PCT-US02-32727-63
C 38	32	2.3	21719	6	US-10-057-498-63
C 39	31.8	2.3	250	5	US-09-531-113-22295
C 40	31.8	2.3	256	5	US-09-531-113-22293
C 41	31.8	2.3	995	6	US-10-316-754-8
C 42	31.8	2.3	1048	6	US-10-144-771-14346
C 43	31.8	2.3	5824	6	US-10-144-771-17297
C 44	31.6	2.2	1077	6	US-10-144-771-43209
C 45	31.6	2.2	1738	6	US-10-348-119-144

ALIGNMENTS

RESULT 1

US-10-293-865-17/c
; Sequence 17, Application US/10293865
; GENERAL INFORMATION:
; APPLICANT: Nikolau, Basil J
; APPLICANT: Wurtele, Eve S
; APPLICANT: Oliver, David J
; APPLICANT: Behal, Robert
; APPLICANT: Schnable, Patrick S
; APPLICANT: Ke, Jinshan
; APPLICANT: Johnson, Jerry L
; APPLICANT: Allred, Carolyn C
; APPLICANT: Fatland, Beth
; APPLICANT: Lutiger, Isabelle
; APPLICANT: Wen, Tsui-Jung
; TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
; TITLE OF INVENTION: Acetyl CoA Levels in Plants
; FILE REFERENCE: 217113
; CURRENT APPLICATION NUMBER: US/10/293,865
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/344,882
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/090,717
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 17
; LENGTH: 2017
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(1000)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1002)...(1508)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1510)...(1519)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1521)...(1531)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1533)...(2017)
US-10-293-865-17

Query Match 2.5%; Score 35.8; DB 6; Length 2017;
Best Local Similarity 54.1%; Pred. No. 3.6;

OY 127 AACTGTGTGAACTCTCAGAACAACTTCTACTACAAACCGCTCCTCTTTCGTGGCTGGA 186
Db 347 ACCTTGCTGTCTCCCTGAGAACGGCTGGTGTGGGACACCGCTGGGCTGCGTGGGAC 406
OY 187 GCTTCTACCTGTATCCC 202
Db 407 GGGTTTAGCGGACGCC 422

RESULT 5
PCT-US02-32727-48/c

; Sequence 48, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shylan
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 48
; LENGTH: 37716
; TYPE: DNA
; ORGANISM: Propionibacterium acnes
PCT-US02-32727-48

Query Match 2.4%; Score 34.4; DB 1; Length 37716;
Best Local Similarity 52.0%; Pred. No. 36;
Matches 77; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

OY 866 ACAAGGACTACGAGCTGAGGCTACCGCTGGAGAGCTGCTACCGCTGGCTAAGCAGTGTA 925
Db 445 ACTCGACAAACCTATCTGCTGGCCATCTTGGTGCGAGTTCCTATCATTTGATAGTGTGTC 386
OY 926 ACATCGCTTCTCTGACGGAACCGCTATCGCTTCTGGAGCTACCAACTACGCTGATCCTGTC 985
Db 385 ATCTCGATGCTCGTTATTGATAAGGTAGGGCGTCGATTCGTTCTTATCACGGGAATATCT 326
OY 986 AGACCGAGTGTCTGAACCTGCTGCTAA 1013
Db 325 ACGATGATTGACGCACTATCGTGCTCA 298

RESULT 6
US-10-057-498-48/c
; Sequence 48, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057.498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 48
; LENGTH: 37716
; TYPE: DNA
; ORGANISM: Propionibacterium acnes
US-10-057-498-48

Query Match 2.4%; Score 34.4; DB 6; Length 37716;
Best Local Similarity 52.0%; Pred. No. 36;
Matches 77; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
OY 866 ACAAGGACTACGAGCTGAGGCTACCGCTGGAGGAGCTGCTACCGCTGGCTAAGCAGTGTA 925
Db 445 ACTCGACAAACCTATCTGCTGGCCATCTTGGTGCGAGTTCCTATCATTTGATAGTGTGTC 386
OY 926 ACATCGCTTCTCTGACGGAACCGCTATCGCTTCTGGAGCTACCAACTACGCTGATCCTGTC 985
Db 385 ATCTCGATGCTCGTTATTGATAAGGTAGGGCGTCGATTCGTTCTTATCACGGGAATATCT 326
OY 986 AGACCGAGTGTCTGAACCTGCTGCTAA 1013
Db 325 ACGATGATTGACGCACTATCGTGCTCA 298

RESULT 7
US-10-144-771-26535
; Sequence 26535, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 26535
; LENGTH: 555
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-26535

Query Match 2.4%; Score 34; DB 6; Length 555;
Best Local Similarity 59.2%; Pred. No. 6.8;
Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 1108 GGAACCGCTACCGCTGATCGCTCAGTGTGCTGTGGAGTGTCTGTGGAAACCGTGTGACC 1167
Db 54 GGAACCTGGTTCACTGCTCATCTCACTCAGTGTGGACAAACCATTTACGAACCAAGGCTTAGC 113
OY 1168 GACGGAAACCACTCTACCTACAAAGCAGGCTGCTCTGA 1205
Db 114 TAAGGAACCATCACCAGTTACACATGAGTTTCTCTGGA 151

RESULT 8
PCT-US02-40225-2140
; Sequence 2140, Application PC/TUS0240225
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS
; FILE REFERENCE: 10182-021-228
; CURRENT APPLICATION NUMBER: PCT/US02/40225
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2140
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
PCT-US02-40225-2140

Query Match 2.4%; Score 34; DB 1; Length 1215;
Best Local Similarity 57.5%; Pred. No. 9.7;
Matches 61; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Db 3506 TTCTACCATGAAGCGCTCCCATTTGGTGAACCGAGTCACTTCCCCAGGC 3458

RESULT 11
US-09-724-676-19769
; Sequence 19769, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19769
; LENGTH: 849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-19769

Query Match 2.4%; Score 33.6; DB 5; Length 849;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 48; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 113 TGGGAACCCCTGTAACCTGTGTGAACCTCTCAGAAGAACTTCTACTACAACAACGCTGCTG 172
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 602 TGGGACTCTCTGCTCCCTTTGTGGCAGCCAGATGGACTGCTGCATGAACAACACAGCTG 661
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 173 CTTTGTGTCCTG 184
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 662 TCTTCTTGCCAG 673
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-724-676A-19769
; Sequence 19769, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19769
; LENGTH: 849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-19769

Query Match 2.4%; Score 33.6; DE 5; Length 849;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 48; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 113 TGGGAACCCCTGTAACCTGTGTGAACCTCTCAGAAGAACTTCTACTACAACAACGCTGCTG 172
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 602 TGGGACTCTCTGCTCCCTTTGTGGCAGCCAGATGGACTGCTGCATGAACAACACAGCTG 661
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 173 CTTTGTGTCCTG 184
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 662 TCTTCTTGCCAG 673
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-620-312D-1053
; Sequence 1053, Application US/09620312D
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Felyan
; APPLICANT: Chen, Rui-hong

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; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 1053
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(1907)
US-09-620-312D-1053

Query Match      2.4%; Score 33.6; DB 5; Length 2161;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 48; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 113 TGGGAACCCCTGCTAACTGTGTGAACCTGCAGAGAAGCTTCTACTACAACACGCTGCTG 172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 568 TGGGACTCTCTGCTCCCTTTGTGGCAGGCCAGATGGACTGCTGCATGAACAACACAGCTG 627

QY 173 CTTTCGTGCGCTG 184
      ||| |||||
Db 628 TCTTCTTGCCAG 639

RESULT 14
PCT-US02-40718-11
; Sequence 11, Application PC/TUS0240718
; GENERAL INFORMATION:
; APPLICANT: Koh, Sang Seok
; APPLICANT: Liu, Qing
; APPLICANT: Chung, Hyun-Ho
; APPLICANT: Zeng, Wen
; APPLICANT: Lee, Bogman
; APPLICANT: Yerramilli, Subrahmanyam
; APPLICANT: Song, Si Young
; APPLICANT: Gene Logic, Inc.
; APPLICANT: LG Chem Ltd.
; TITLE OF INVENTION: GENE EXPRESSION PROFILES IN LIVER DISEASE
; FILE REFERENCE: 44921-5109-WO
; CURRENT APPLICATION NUMBER: PCT/US02/40718
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,815
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/343,185
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2194
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. Z48475

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PCT-US02-40718-11
Query Match      2.4%; Score 33.6; DB 1; Length 2194;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 48; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 113 TGGGAACCCCTGCTAACTGTGTGAACCTGCAGAGAAGCTTCTACTACAACACGCTGCTG 172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 602 TGGGACTCTCTGCTCCCTTTGTGGCAGGCCAGATGGACTGCTGCATGAACAACACAGCTG 661

QY 173 CTTTCGTGCGCTG 184
      ||| |||||
Db 662 TCTTCTTGCCAG 673

RESULT 15
US-09-620-312D-1052
; Sequence 1052, Application US/09620312D
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 1052
; LENGTH: 2230
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(1976)
US-09-620-312D-1052

Query Match      2.4%; Score 33.6; DB 5; Length 2230;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 48; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 113 TGGGAACCCCTGCTAACTGTGTGAACCTGCAGAGAAGCTTCTACTACAACACGCTGCTG 172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 637 TGGGACTCTCTGCTCCCTTTGTGGCAGGCCAGATGGACTGCTGCATGAACAACACAGCTG 696

QY 173 CTTTCGTGCGCTG 184
      ||| |||||
Db 697 TCTTCTTGCCAG 708

Search completed: February 17, 2003, 01:57:28
Job time : 308.042 secs

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